

Phylogeographic patterns of *Escherichia coli* isolated from white-tailed deer, *Odocoileus virginianus*, during necropsy in farmed deer surveillance program

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White-tailed deer (*Odocoileus virginianus*) (WTD) farms are distributed throughout Florida and number nearly 400. The Cervidae Health Research Initiative (CHeRI) is an initiative that investigates disease and health of farmed cervids statewide. Within the Florida industry, Epizootic Hemorrhagic disease virus (EHDV) and Bluetongue virus (BTV) are major causes of disease and associated economic losses. Often, deer survive EHDV or BTV infections but succumb to secondary bacterial infections, including *Escherichia coli*. *E. coli* can be opportunistic with severe illness or death occurring in hosts weakened from viral infection. We investigated presumptive *E. coli* strains isolated from WTD during necropsy investigations. Genomic DNA was extracted and whole genome sequenced from 61 suspect *E. coli* isolates. Exploratory spatial data analysis (ESDA) of the distribution of *E. coli* phylotypes, distribution of *E. coli*, and deer between ranches was performed. We examined phylogenetic relationships between isolates, categorized by ranch and year and compared to all reported *E. coli* isolates in Florida from EnteroBase. One strain was *Enterobacter hormaechei* and the other 60 were *E. coli*. Two strains were toxigenic. Deer isolates represented 7 phylogroups with B1 being the most prevalent (45/60) and geographically widespread (14/16 counties reporting *E. coli*). Phylogroup A was the second most prevalent phylogroup. In at least two instances two phylogroups were present within a single animal. We found that deer isolates spanned many of known phylotypes in Florida from animals and humans. Diversity patterns suggest animals are infected locally with most animals on ranches having high genomic similarity within phylogroups.

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